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# OM protein - protein search, using sw model

Run on: June 21, 2002, 08:25:26 ; Search time 22.96 Seconds

(without alignments)  
141.657 Million cell updates/sec

Title: US-09-351-778a-12

Sequence: 1 MTCSTIAPTDTYRNTATGL.....NEKIHRLDLKPCSLLOYD 84

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 105224 seqs, 38719550 residues

Word size : 0

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : SWISSPROT\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	66.7	101	E311_ADE02	P24935 human adeno
2	56	66.7	101	E311_ADE06	O55653 human adeno
3	19	22.6	93	E311_ADE05	P17590 human adeno
4	6	7.1	92	HRK_MOUSE	F70678 mus musculu
5	6	7.1	121	VMBF_POPMV	002123 poplar mosa
6	6	7.1	126	NIEW_FRASE	002570 frankia sp.
7	6	7.1	136	YRNE_CAEEL	009420 caenorhabdl
8	6	7.1	142	YB9E_YEAST	P38337 saccharomyc
9	6	7.1	151	FER8_METVA	O57619 methanococc
10	6	7.1	152	RK34_SPIOL	P82244 splinacia ol
11	6	7.1	157	HES2_MOUSE	O54792 mus musculu
12	6	7.1	157	HES2_RAT	P35429 mus musculu
13	6	7.1	173	HES2_HUMAN	O93543 homo sapien
14	6	7.1	184	YEB8_HAEIN	P44215 haemophilus
15	6	7.1	194	IM22_HUMAN	O93544 homo sapien
16	6	7.1	195	NRTN_MOUSE	P97463 mus musculu
17	6	7.1	217	RPE_HELPY	O92175 helicobacte
18	6	7.1	217	RPE_HELPY	P56188 helicobacte
19	6	7.1	227	IDLI_MOUSE	P58044 mus musculu
20	6	7.1	240	45KD_TAEVO	P19617 taenia ovis
21	6	7.1	240	PYRH_AQUAE	O66929 aquifex aeo
22	6	7.1	248	RIBF_RHOOP	O84990 rhodococcus
23	6	7.1	248	VGL2_EBV	P03218 Epstein-ba
24	6	7.1	263	V225_METVA	O57678 methanococc
25	6	7.1	280	HESI_HUMAN	O14469 mus musculu
26	6	7.1	281	HESI_RAT	O04666 ratus norv
27	6	7.1	282	HESI_MOUSE	P35428 mus musculu
28	6	7.1	290	HESI_CHICK	O57337 gallus gall
29	6	7.1	304	PTPR_BACAM	P11029 bacillus am
30	6	7.1	316	MHPF_ECOLI	P77560 escherichia
31	6	7.1	318	FEPE_ECOLI	P38844 saccharomyc
32	6	7.1	325	YH03_YEAST	
33	6	7.1	328	IRL1_HUMAN	O01638 homo sapien

## ALIGNMENTS

RESULT	ID	E311_ADE02	STANDARD:	PRT:	101 AA.
AC	P24935:				
DT	01-MAR-1992 (Rel. 21, Created)				
DT	01-MAR-1992 (Rel. 21, Last sequence update)				
DT	01-DEC-1992 (Rel. 24, Last annotation update)				
DE	Early E3A 11.6 kDa glycoprotein.				
OS	Human adenovirus type 2.				
OC	Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.				
OX	NCBI_Taxid=10515;				
RP	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=81053687; PubMed=6253880;				
RA	Herlisse J., Courtois G., Galibert F.;				
RT	"Nucleotide sequence of the Ecore D fragment of adenovirus 2 genome.";				
RL	Nucleic Acids Res. 8:2173-2192(1980).				
RU	[2]				
RP	IDENTIFICATION OF PROTEIN.				
RX	MEDLINE=93079877; PubMed=1448922;				
RA	Scaria A., Tollefsen A.E., Saha S.K., Wold W.S.M.;				
RT	"The E3-11.6K protein of adenovirus is an Asn-glycosylated integral membrane protein that localizes to the nuclear membrane.";				
RL	Virology 191:743-753(1992)				
CC	-1- SUBCELLULAR LOCATION: INTEGRAL NUCLEAR MEMBRANE PROTEIN.				
CC	-1- PTM: N-GLYCOSYLATED AND PROBABLY ALSO O-GLYCOSYLATED.				
CC	-1- SIMILARITY: BELONGS TO A FAMILY THAT GROUP TOGETHER AD2 E3A 11.6 kDa, AD5 E3A 10.5 kDa, AD3 E3 9 kDa, AND AD7 E3 7.7 kDa.				
CC	-----				
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb.ch/announce/">http://www.isb.ch/announce/</a> or send an email to <a href="mailto:license@isb.slb.ch">license@isb.slb.ch</a> ).				
CC	-----				
DR	EMBL: J01917; AAA92222.1;				
KW	Early protein; Glycoprotein; Transmembrane.				
FT	TRANSMEM 41 62				
FT	CARBOHYD 14 14 N-LINKED (GLCNAC ...) (POTENTIAL).				
FT	SEQUENCE 101 AA; 11644 MW; FB89FC66921B84B CMC64;				

Query Match 66.74; Score 56; DB 1; Length 101;  
Best Local Similarity 100.0%; Pred. No. 5.2e-53;  
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy	29	IALMPFCIIIMWLICCKRRARPRPIYIVNPNKIHRLDGLKPCSLLOYD 84
Db	46	IALMPFCIIIMWLICCKRRARPRPIYIVNPNKIHRLDGLKPCSLLOYD 101
RESULT	2	
E311_ADE06		
ID	E311_ADE06	STANDARD: PRT: 101 AA.

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AC 055653;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Early E3A 11.6 kDa glycoprotein.
OS Human adenovirus type 6.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
ON NCBI_TaxID=10534;
RN [1]
RP SEQUENCE FROM N.A.
RA Reichmann H., Scharschmidt E., Geisler B., Hausmann J., Ottmann D.,
RA Bauer U., Flunker G., Seidel W.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL NUCLEAR MEMBRANE PROTEIN.
CC -1- PTM: N-GLYCOSYLATED AND PROBABLY ALSO O-GLYCOSYLATED (BY
CC SIMILARITY).
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT TOGETHER AD2 E3A 11.6
CC kDa, AD5 E3A 10.5 kDa, AD3 E3 9 kDa, AND AD7 E3 7.7 kDa.
CC
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CC -----
CC EMBL: Y16037; CAA75991.1; TRANSMEMBRANE.
CC KW TRANSMEM 41 62 POTENTIAL.
CC FT CARBOHYD 14 14 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SO SEQUENCE 101 AA; 11613 MW; EF21900939E3B4B CRC64;

Query Match 56.7%; Score 56; DB 1; Length 101;
Best Local Similarity 100.0%; Pred. No. 5; 2e-53; Indels 0; Gaps 0;
Matches 36; Conservative 0; Mismatches 0;

QY 29 IALMFVCLIMMLICLRRARRAPPIVPIIPLNPHNEKTHRLDGLKPCSLLOYD 84
DB 46 IALMFVCLIMMLICLRRARRAPPIVPIIPLNPHNEKTHRLDGLKPCSLLOYD 101

RESULT 3
E31L_ADE05 STANDARD; PRT; 93 AA.
AC P17590;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Early E3A 10.5 kDa glycoprotein.
OS Human adenovirus type 5.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
ON NCBI_TaxID=28285;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=85092338; PubMed=2981456;
RA Cladarias C., Mold W.S.M.;
RT "DNA sequence of the early E3 transcription unit of adenovirus 5."
RL Virology 140:28-43(1985).
RN [2]
RP COMPLETE GENOME.
RA MEDLINE=92087470; PubMed=1727603;
RA Chroboczek J., Bieker F., Jactot B.;
RT "The sequence of the genome of adenovirus type 5 and its comparison
RT with the genome of adenovirus type 2."
RL Virology 186:280-285(1992).
CC -1- SUBCELLULAR LOCATION: INTEGRAL NUCLEAR MEMBRANE PROTEIN.
CC -1- PTM: N-GLYCOSYLATED AND PROBABLY ALSO O-GLYCOSYLATED.
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT TOGETHER AD2 E3A 11.6
CC kDa, AD5 E3A 10.5 kDa, AD3 E3 9 kDa, AND AD7 E3 7.7 kDa.
CC
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CC -----
CC EMBL: M73260; NOT_ANNOTATED_CDS.
CC DR EMBL: X03002; CAA26784.1;
CC DR PIR: A05245; ERAD53.
CC KW Early protein; Glycoprotein; Transmembrane.
CC FT TRANSMEM 34 55 POTENTIAL.
CC FT CARBOHYD 3 3 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SO SEQUENCE 93 AA; 10523 MW; 008AD087AAB45A8F CRC64;

Query Match 22.6%; Score 19; DB 1; Length 93;
Best Local Similarity 100.0%; Pred. No. 2; 4e-13; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0;

QY 29 IALMFVCLIMMLICLRR 47
DB 39 IALMFVCLIMMLICLRR 57

RESULT 4
HRK_MOUSE STANDARD; PRT; 92 AA.
ID HRK_MOUSE
AC P70578;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Activator of apoptosis harakiri (Neuronal death protein DP5).
GN HRK OR DP5 OR BID3.
OS Mus musculus (Mouse), and
OS Rattus norvegicus (Rat).
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
ON NCBI_TaxID=10090, 10116;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Brain;
RA Imaizumi K.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: ACTIVATES APOPTOSIS AND INTERACTS SELECTIVELY WITH
CC SURVIVAL-PROMOTING PROTEINS BCL-2 AND BCL-XL (BY SIMILARITY).
CC -1- DOMAIN: THE BH3 DOMAIN IS REQUIRED FOR THE INDUCTION OF CELL
CC DEATH (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC
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CC -----
CC EMBL: D83697; BA12065.1;
CC DR EMBL: D83698; BA12066.1;
CC DR MGD: MG1:1201608; BID3.
CC DR InterPro: IPR000712; BCL_2.
CC DR PROSITE: PS01259; BH3; 1.
CC KW Apoptosis.
CC FT DOMAIN 33 47 BH3.
CC SO SEQUENCE 92 AA; 10078 MW; 95760B9EAE88F1DE CRC64;

Query Match 7.1%; Score 6; DB 1; Length 92;
Best Local Similarity 100.0%; Pred. No. 21; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

QY 47 RRRARP 52

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DB      50 RRRARP 55

RESULT  5
VMBP_POPMV STANDARD: PRT: 121 AA.
ID VMBP_POPMV 002123;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-OCT-1993 (Rel. 27, Last annotation update)
DE 14 kDa protein (Putative nucleic acid-binding protein).
OS Poplar mosaic virus (isolate ATCC PV275) (PMV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus.
NC NCB1_TaxID=31709;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92333281; PubMed=1629709;
RA Henderson J., Glibbs M.J., Edwards M.L., Clarke V.A., Gardner K.A.,
RA Cooper J.I.;
RT "Partial nucleotide sequence of poplar mosaic virus RNA confirms its
RT classification as a Carlavirus."
RL J. Gen. Virol. 73:1887-1890(1992).
CC -1- FUNCTION: MAY ACT AS A REGULATORY FACTOR DURING VIRAL
CC TRANSCRIPTION.
CC -1- SIMILARITY: TO NUCLEIC ACID-BINDING PROTEINS FROM OTHER
CC CARLAVIRUSES.
CC -----
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CC -----
DR EMBL: X65102; CAA46327.1; -
DR EMBL: D13364; BAA02629.1; -
DR PIR: J01646; J01646.
DR PIR: S23876; S23876.
DR InterPro: IPR002568; Carla_C4.
DR Pfam: PF01623; Carla_C4; 1.
DR Zinc-finger; DNA-binding.
FT ZN_FING 62
FT 83
SQ SEQUENCE 121 AA; 14451 MW; 705205527BF7D3CF CRC64;

Query Match
Best Local Similarity 7.1%; Score 6; DB 1; Length 121;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 46 KRRRAR 51
DB 52 KRRRAR 57

RESULT 6
NIFM_FRASE STANDARD: PRT: 126 AA.
ID NIFM_FRASE 0925Y0;
AC 0925Y0;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Nitrogenase stabilizing/protective protein nifm.
GN NIFM.
OS Frankia sp. (strain EuIK1).
OC Bacteria; Firmicutes; Actinobacteriia; Actinobacteridae;
OC Actinomycetales; Frankineae; Frankiaceae; Frankia.
NC NCB1_TaxID=47227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-EuIK1;
RA Chung-Sun A., Ji-Tae K., Won-Jin K., Won-Young Y.;

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RT "Nif gene organization and nucleotide sequences from Frankia EuIK1
RT strain."
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: May protect the nitrogenase Fe-Mo protein from oxidative
CC damage (By similarity).
CC -1- SUBUNIT: Homotrimer; associates with nifD (By similarity).
CC -1- SIMILARITY: BELONGS TO THE NIFM FAMILY.
CC -----
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CC -----
DR EMBL: AF119361; AAD17267.1; -
DR Nifrogen fixation.
KW Nifrogen fixation.
SQ SEQUENCE 126 AA; 14287 MW; 295D8C9102FD317E CRC64;

Query Match
Best Local Similarity 7.1%; Score 6; DB 1; Length 126;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 TTATGL 20
DB 80 TTATGL 85

RESULT 7
YRN6_CAEEL STANDARD: PRT: 136 AA.
ID YRN6_CAEEL 009420;
AC 009420;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Hypothetical 14.2 kDa protein R07B1.6 in chromosome X.
GN R07B1.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Rhabditidae; Caenorhabditis.
NC NCB1_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Kershaw J.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
DR EMBL: Z48621; CAA8543.1; -
DR Wormpep: R07B1.6; CE01632.
DR InterPro: IPR002601; C6.
DR Pfam: PF01681; C6; 1.
KW Hypothetical protein.
SQ SEQUENCE 136 AA; 14169 MW; D7F47A83F3F81787 CRC64;

Query Match
Best Local Similarity 7.1%; Score 6; DB 1; Length 136;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TTAFTT 10
DB 31 TTAFTT 36

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RESULT 8
RT 1B9E_YEAST STANDARD: PRT: 142 AA.
AC P38137:
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 13-JUL-1998 (Rel. 36, Last annotation update)
DE Hypothetical 16.4 kDa protein in POP4-SHM1 intergenic region.
GN YBR258C OR YBR1726.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
  Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-S288C;
RX MEDLINE=93220397; PubMed=8465606;
RA Daignon F., Bileau N., Crouzet M., Aigle M.;
RT "The complete sequence of a 19,482 bp segment located on the right
  arm of chromosome II from Saccharomyces cerevisiae.";
RL Yeast 9:189-199(1993).
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CC
CC EMBL: X70529; CAA49922.1;
CC DR EMBL: Z36127; CAA85221.1;
CC DR PIR: S32960; S32960
CC SCD: S0000462; YBR258C.
CC DR SCD: S0000462; YBR258C.
CC Hypothetical protein.
SQ SEQUENCE 142 AA; 16429 MW; 12E73FC3DD22507 CRC64;

Query Match
Best Local Similarity 7.1%; Score 6; DB 1; Length 142;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 19 GLTSL 24
DB 71 GLTSL 76

RESULT 9
RT 1B9E_YEAST STANDARD: PRT: 151 AA.
AC 057619;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative ferredoxin M0155.
GN M0155.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
  Methanococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
  Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
  Kertland A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
  Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
  Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhmann J.L., Nguyen D.,
  Ullrich T.R., Kelley J.M., Peterson J.D., Sedow P.W., Hanna M.C.,
  Cotton M.D., Roberts K.M., Hirst M.A., Kalne B.P., Borodovsky M.,
  Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

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RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
  jannaschii.";
RL Science 273:1058-1073(1996).
CC -1- COFACTOR: BINDS 1 4FE-4S CLUSTER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE BACTERIAL TYPE FERREDOXIN FAMILY.
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CC
CC EMBL: U67472; AAB98137.1;
CC DR HSP: P00195; 1CLF.
CC DR TIGR: M0155;
CC DR InterPro: IPR001450; 4FE4S-ferredoxin.
CC DR Pfam: PF00037; Fer4. 1.
CC DR PRINTS: PR00353; 4FE4S-FERREDOXIN.
CC DR PROSITE: PS00198; 4FE4S-FERREDOXIN; 1.
CC KM Hypothetical protein; Electron transport; 4Fe-4S; Iron-sulfur;
  Complete proteome.
CC FT METAL 73 73 IRON-SULFUR (4FE-4S) (POTENTIAL).
CC FT METAL 76 76 IRON-SULFUR (4FE-4S) (POTENTIAL).
CC FT METAL 79 79 IRON-SULFUR (4FE-4S) (POTENTIAL).
CC FT METAL 82 83 IRON-SULFUR (4FE-4S) (POTENTIAL).
SQ SEQUENCE 151 AA; 16985 MW; 86C9B27DEFAEAF1 CRC64;

Query Match
Best Local Similarity 7.1%; Score 6; DB 1; Length 151;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 58 IIVLNP 63
DB 5 IIVLNP 10

RESULT 10
RT RK34_SPIOI STANDARD: PRT: 152 AA.
AC P82244;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 50S ribosomal protein L34, chloroplast precursor.
GN RPL34.
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  Caryophyllales; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE FROM N.A.; SEQUENCE OF 92-101, AND MASS SPECTROMETRY.
RC STRAIN=CV, ALMARO; TISSUE=Leaf;
RX MEDLINE=20435798; PubMed=10874046;
RA Yamauchi K., Subramanian A.R.;
RT "The plastid ribosomal proteins. Identification of all the proteins in
  the 50 S subunit of an organelle ribosome (chloroplast).";
RL J. Biol. Chem. 275:28466-28482(2000).
CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
CC -1- SUBCELLULAR LOCATION: Chloroplast.
CC -1- TISSUE SPECIFICITY: UBQUITOUS.
CC -1- MASS SPECTROMETRY: MW=6767.1; METHOD=Electrospray; RANGE=92-152.
CC -1- SIMILARITY: BELONGS TO THE L34P FAMILY OF RIBOSOMAL PROTEINS.
-----
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DR EMBL: AF238221; AAF64157.1; -  
 DR InterPro: IPR000771; Ribosomal\_L34.  
 DR Pfam: PF00468; Ribosomal\_L34; 1.  
 DR PROSITE: PS00784; RIBOSOMAL\_L34; FALSE\_NEG.  
 KM Ribosomal protein; Chloroplast; Transit peptide; rRNA-binding.  
 FT TRANSIT 1 91  
 FT CHAIN 92 152  
 FT SEQUENCE 152 AA; 16095 MW; 755A990D441ADB18 CRC64.

Query Match 7.18; Score 6; DB 1; Length 152;  
 Best Local Similarity 100.0%; Pred. No. 33;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 45 LKRRRA 50  
 |||||  
 Db 127 LKRRRA 132

RESULT 11  
 HES2\_MOUSE  
 ID HES2\_MOUSE STANDARD; PRT; 157 AA.  
 AC 054792;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Transcription factor HES-2 (Hairy and enhancer of split 2).  
 GN HES2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.  
 NC NCBL\_TaxID-10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-129/J;  
 RX MEDLINE-98234545; PubMed-9570950;  
 RA Nishimura M., Isaka F., Ishibashi M., Tomita K., Tsuda H.,  
 RA Nakanishi S., Kageyama R.;  
 RT Structure, chromosomal locus, and promoter of mouse Hes2 gene, a  
 RT homologue of Drosophila hairy and enhancer of split.;  
 RL Genomics 49:69-75(1998).  
 CC -1- FUNCTION: TRANSCRIPTIONAL REPRESSOR OF GENES THAT REQUIRE A BHLH  
 CC PROTEIN FOR THEIR TRANSCRIPTION.  
 CC -1- SUBUNIT: TRANSCRIPTION REPRESSION REQUIRES FORMATION OF A COMPLEX  
 CC WITH A CO-REPRESSOR PROTEIN (GROUCHO).  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- DOMAIN: HAS A PARTICULAR TYPE OF BASIC DOMAIN (PRESENCE OF A  
 CC HELIX-INTERRUPTING PROLINE) THAT BINDS TO THE N-BOX (CACNAG),  
 CC RATHER THAN THE CANONICAL E-BOX (CANNTG).  
 CC -1- DOMAIN: THE CARBOXYL-TERMINAL WRPW MOTIF IS A TRANSCRIPTIONAL  
 CC REPRESSION DOMAIN NECESSARY FOR THE INTERACTION WITH GROUCHO. A  
 CC TRANSCRIPTIONAL CO-REPRESSOR RECRUITED TO SPECIFIC TARGET DNA BY  
 CC HAIRY-RELATED PROTEINS.  
 CC -1- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF  
 CC TRANSCRIPTION FACTORS. "HAIRY" SUBFAMILY.  
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DR EMBL: AB009967; BAA24091.1; -  
 DR MGD: MGI:1098624; Hes2.  
 DR InterPro: IPR001015; HLH\_MYC.  
 DR InterPro: IPR001092; HLH\_dlm.  
 DR InterPro: IPR003650; Orange.  
 DR Pfam: PF00010; HLH; 1.  
 DR SMART: SM00353; HLH; 1.

DR SMART: SM00511; ORANGE; 1  
 DR PROSITE: PS00038; HELIX-LOOP-HELIX; 1.  
 KM Transcription regulation; DNA-binding; Nuclear protein; Repressor.  
 FT DNA\_BIND 13 26  
 FT BASIC DOMAIN.  
 FT TRANSIT 27 71  
 FT HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).  
 FT DOMAIN 139 148  
 FT PRO-RICH.  
 FT WRPW MOTIF (REQUIRED FOR ACTIVITY)  
 FT DOMAIN 154 157  
 FT (BY SIMILARITY).  
 FT SEQUENCE 157 AA; 17231 MW; 570A0C67F4992EAV7 CRC64.

Query Match 7.18; Score 6; DB 1; Length 157;  
 Best Local Similarity 100.0%; Pred. No. 34;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 46 KRRRAR 51  
 |||||  
 Db 23 KRRRAR 28

RESULT 12  
 HES2\_RAT  
 ID HES2\_RAT STANDARD; PRT; 157 AA.  
 AC P35429;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Transcription factor HES-2 (Hairy and enhancer of split 2).  
 GN HES2 OR HES-2.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.  
 NC NCBL\_TaxID-10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Embryonic brain;  
 RX MEDLINE-93358886; PubMed-8354270;  
 RA Ishibashi M., Sasai Y., Nakanishi S., Kageyama R.;  
 RT Molecular characterization of HES-2, a mammalian helix-loop-helix  
 RT factor structurally related to Drosophila hairy and enhancer of  
 RT split.;  
 RL Eur. J. Biochem. 215:645-652(1993).  
 CC -1- FUNCTION: TRANSCRIPTIONAL REPRESSOR OF GENES THAT REQUIRE A BHLH  
 CC PROTEIN FOR THEIR TRANSCRIPTION.  
 CC -1- SUBUNIT: TRANSCRIPTION REPRESSION REQUIRES FORMATION OF A COMPLEX  
 CC WITH A CO-REPRESSOR PROTEIN (GROUCHO).  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- DOMAIN: HAS A PARTICULAR TYPE OF BASIC DOMAIN (PRESENCE OF A  
 CC HELIX-INTERRUPTING PROLINE) THAT BINDS TO THE N-BOX (CACNAG),  
 CC RATHER THAN THE CANONICAL E-BOX (CANNTG).  
 CC -1- DOMAIN: THE CARBOXYL-TERMINAL WRPW MOTIF IS A TRANSCRIPTIONAL  
 CC REPRESSION DOMAIN NECESSARY FOR THE INTERACTION WITH GROUCHO. A  
 CC TRANSCRIPTIONAL CO-REPRESSOR RECRUITED TO SPECIFIC TARGET DNA BY  
 CC HAIRY-RELATED PROTEINS.  
 CC -1- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF  
 CC TRANSCRIPTION FACTORS. "HAIRY" SUBFAMILY.  
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DR EMBL: D14029; BAA03118.1; -  
 DR PIR: S35037; S35037.  
 DR TRANSFAC: T01650; -  
 DR InterPro: IPR001015; HLH\_MYC.  
 DR InterPro: IPR001092; HLH\_dlm.  
 DR InterPro: IPR003650; Orange.  
 DR Pfam: PF00010; HLH; 1.  
 DR SMART: SM00353; HLH; 1.

DR SMART: SM00511: ORANGE; 1.  
 DR PROSITE: PS00038: HELIX\_LOOP\_HELIX; 1.  
 KW Transcription regulation; DNA-binding; Nuclear protein; Repressor.  
 FT DNA\_BIND 13 26 BASIC DOMAIN.  
 FT DOMAIN 27 71 HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).  
 FT DOMAIN 139 148 PRO-RICH.  
 FT DOMAIN 154 157 WRPW MOTIF (REQUIRED FOR ACTIVITY)  
 (BY SIMILARITY).  
 FT SEQUENCE 157 AA: 17028 MW: B5D621E814AE0369 CRC64:

Query Match 7.1%; Score 6; DB 1; Length 157;  
 Best Local Similarity 100.0%; Pred. No. 34;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 46 KRRRAR 51  
 |||||  
 DB 23 KRRRAR 28

RESULT 13  
 HES2\_HUMAN STANDARD: PRT; 173 AA.  
 AC 09Y543; 09Y542;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Transcription factor HES-2 (Hairy and enhancer of split 2).  
 GN HES2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 RX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Howden P.;  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: TRANSCRIPTIONAL REPRESSOR OF GENES THAT REQUIRE A BHLH  
 PROTEIN FOR THEIR TRANSCRIPTION (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Nuclear (BY SIMILARITY).  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: 1 (SHOWN HERE) AND 2; MAY BE  
 PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- DOMAIN: HAS A PARTICULAR TYPE OF BASIC DOMAIN (PRESENCE OF A  
 HELIX-INTERUPTING PROLINE) THAT BINDS TO THE N-BOX (CACNAG),  
 RATHER THAN THE CANONICAL E-BOX (CANNTG).  
 CC -1- DOMAIN: THE CARBOXY-TERMINAL WRPW MOTIF IS A TRANSCRIPTIONAL  
 REPRESSION DOMAIN NECESSARY FOR THE INTERACTION WITH GRCUCHO, A  
 TRANSCRIPTIONAL CO-REPRESSOR RECRUITED TO SPECIFIC TARGET DNA BY  
 HAIRY-RELATED PROTEINS (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF  
 TRANSCRIPTION FACTORS. "HAIRY" SUBFAMILY.

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CC EMBL: AL031848; CAB46198.1; -  
 DR EMBL: AL031848; CAB46199.1; -  
 DR InterPro: IPR003015; HLH\_MYC.  
 DR InterPro: IPR001092; HLH\_dim.  
 DR InterPro: IPR003650; Orange.  
 DR Pfam: PF000010; HLH; 1.  
 DR SMART: SM00511; ORANGE; 1.  
 DR PROSITE: PS00038; HELIX\_LOOP\_HELIX; 1.  
 KW Transcription regulation; DNA-binding; Nuclear protein; Repressor;  
 KW Alternative splicing.  
 FT DNA\_BIND 13 26 BASIC DOMAIN.  
 FT DOMAIN 27 71 HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).

FT DOMAIN 139 167 PRO-RICH.  
 FT DOMAIN 170 173 WRPW MOTIF (REQUIRED FOR ACTIVITY)  
 (BY SIMILARITY).  
 FT VARSPIC 48 173 NSNCSKLEKADVLEMTVFLELPASSWPTAAPPCDSYRE  
 GYSACVARLARLVPCRVLEPAPASVRLLEMRPAASATLD  
 GGRAGDSGSAVPAPAPASAPAPAPAPSPSPPCPGILM  
 RPW -> DASGHWHTPLPLHAQNCFLFYIQAEQPPA (IN  
 ISOFORM 2).  
 FT SEQUENCE 173 AA: 18470 MW: B3751F4576E84F3D CRC64:

Query Match 7.1%; Score 6; DB 1; Length 173;  
 Best Local Similarity 100.0%; Pred. No. 36;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 46 KRRRAR 51  
 |||||  
 DB 23 KRRRAR 28

RESULT 14  
 YE89\_HAEIN STANDARD: PRT; 184 AA.  
 AC P44215;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical protein H11489.  
 GN H11489.  
 OS Haemophilus influenzae.  
 CC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;  
 CC Haemophilus.  
 RX NCBI\_Taxid=727;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN RD / KW20 / ATCC 51907;  
 RC MEDLINE-95350630; PubMed-7542800.  
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,  
 RA Kelleys A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,  
 RA McCreney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,  
 RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,  
 RA Wetman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,  
 RA Uetshack T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,  
 RA Fine L.D., Fritchman J.L., Fuhmann J.L., Geoghegan N.S.M.,  
 RA Gnehm C.U., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,  
 RA Venter J.C.;  
 RT "Whole-genome random sequencing and assembly of Haemophilus  
 influenzae Rd.";  
 RL Science 269:496-512(1995).

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CC EMBL: U32826; AAC3143.1; -  
 DR TIGR: H11489; -  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 184 AA: 20782 MW: C298357DBED80211 CRC64:

Query Match 7.1%; Score 6; DB 1; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 38;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 76 PCSILL 81  
 |||||  
 DB 73 PCSILL 78

```

RESULT 15
IM22_HUMAN STANDARD: PRT; 194 AA.
ID IM22_HUMAN
AC Q9Y584;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Mitochondrial import inner membrane translocase subunit TIM22.
GN TIM22 OR TIM22.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N. A.
RA Bauer M.F., Brunner M., Neupert W., Gerblitz K.-D., Hofmann S.;
RT Cloning and mapping of human Tim22, homologous to S.cerevisiae Tim22,
RT a membrane-integrated component of the Tim22-54 machinery for the
RT import of mitochondrial carrier proteins."
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: ESSENTIAL COMPONENT OF MITOCHONDRIAL INNER MEMBRANE
CC PROTEIN IMPORT PATHWAY. INVOLVED IN THE IMPORT OF PROTEINS
CC TARGETED TO THE INNER MEMBRANE OF THE MITOCHONDRION SUCH AS
CC MITOCHONDRIAL CARRIER FAMILY MEMBERS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC INNER MEMBRANE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TIM17/TIM22/TIM23 FAMILY.
CC -----
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CC -----
DR EMBL; AF155330; AAD40106.1; -.
DR InterPro; IPR003397; TIM17.
DR Pfam; PF02466; TIM17; 1.
KM Protein transport; Transmembrane; Mitochondrion; Inner membrane.
FT TRANSMEM 74 94 POTENTIAL.
FT TRANSMEM 123 143 POTENTIAL.
FT TRANSMEM 170 190 POTENTIAL.
SQ SEQUENCE 194 AA; 20270 MW; DC986E23DDF18377 CRC64;

Query Match 7.1%; Score 6; DB 1; Length 194;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 78 SLLLOV 83
DB 26 SLLLOV 31

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